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APPENDIX A

<u>Alignment of maize CesA proteins</u> The common motifs (D, D, and QXXRW) are marked with an asterisk on top. These motifs are found in all processive beta-glycosyltransferases (Saxena et al., 1995, Multidomain architecture of beta-glycosyltransferases: implications for mechanism of action, J. Bacteriol. 177:1419-1424). Aside from these motifs, many other domains are completely conserved among dicot (Arabidopsis) and monocot (maize) CesA proteins.

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                              1                                             50
ZmCesA9      (1)  --------------------------MEGDADGVKSGRRGGGQVCQICGDG
ZmCesA8      (1)  ---MEASAGLVAGSHNRNELVVIRRDRESGAAGGGAARRAEAPCQICGDE
ZmCesA7      (1)  ---MEASAGLVAGSHNRNELVVIRRDGDP--GPKPPREQNGQVCQICGDD
ZmCesA6      (1)  -----------------------------MDQRNGQVCQICGDD
ZmCesA5      (1)  --------------------------MDGGDATNSGKHVAGQVCQICGDG
ZmCesA4      (1)  --------------------------MEGDADGVKSGRRGGGQVCQICGDG
ZmCesA3      (1)  ----------------------------------------------------
ZmCesA2      (1)  ---MAANKGMVAGSHNRNEFVMIRHDGDAPVPAKPTKSANGQVCQICGDT
SEQIDNO.30   (1)  ---MEASAGLVAGSHNRNELVLIRGHEDP-----KPLRALSGQVCEICGDE
ZmCesA12     (1)  -----------------------------------MMESAAAQSCAACGDD
ZmCesA11     (1)  ---------------------------MDAGSVTGGLAAGSHMRDELHVMRAREEP---NAKVRSADVKTCRVCADE
ZmCesA10     (1)  MDAGSVTGGLAAGSHMRDELHVMRAREEP---NAKVRSADVKTCRVCADE
ZmCesA1      (1)  ---MAANKGMVAGSHNRNEFVMIRHDGDVPGSAKPTKSANGQVCQICGDS
Consensus    (1)                              D           R   GQVCQICGD
                              51                                            100
ZmCesA9      (26) VGTTAEGDVFTACDVCGFPVCRPCYEYERKDGTQACPQCKNKYKRHKGSP
ZmCesA8      (48) VGVGFDGEPFVACNECAFPVCRACYEYRRREGSQACPQCRTRYKRLKGCP
ZmCesA7      (46) VGLAPGGDPFVACNECAFPVCRDCYEYERRECTQNCPQCKTRYKRLKGCQ
ZmCesA6      (16) VGRNPDGEPFVACNECAFPICRDCYEYERREGTQNCPQCKTRFKRFKGCA
ZmCesA5      (25) VGTAADGDLFTACDVCGFPVCRPCYEYERKDCTQACPQCKTKYKRHKGSP
ZmCesA4      (26) VGTTAEGDVFAACDVCGFPVCRPCYFYERKDGTQACPQCKTKYKRHKGSP
ZmCesA3      (1)  ----------------------------------------------------
ZmCesA2      (48) VGVSATGDVFVACNECAFPVCRPCYEYERKEGNQCCPQCKTRYKRQKGSP
SeqIdNo.30   (44) VGLTVDGDLFVACNECGFPVCRPCYRYERREGTQNCPQCKTRYKRLKGSP
ZmCesA12     (1)  ----------------------------------------------------
ZmCesA11     (17) AR--------AACRACSYALCRACLDEDAAEGRTTCARCGGDYAAINPAR
ZmCesA10     (48) VGTREDGQPFVACAECGFPVCRPCYEYERSEGTQCCPQCNTRYKRQKCCP
ZmCesA1      (48) VGVSATGDVFVACNECAFPVCRPCYEYERKEGNQCCPQCKTRYKRQKGSP
Consensus    (51) VG    DGD FVAC ECAFPVCRPCYEYERKEGTQ CPQCKTRYKR KGSP
                              101                                           150
ZmCesA9      (76) AIRGEE-GDDTDADDASDFNYPASGND------DQKQKIADRMRSWRMNA
ZmCesA8      (98) RVAGDE-EEDGVDDLEGEFGLQDGAAHE-----DDPQYVAESMIRAQMSY
ZmCesA7      (96) RVTGDE-EEDGVDDLENEFNWDG----------HDSQSVAESMLYGHMSY
ZmCesA6      (66) RVPGDE-EEDGVDDLENEFNWSDK---------HDSQYLAESMLHAHMSY
ZmCesA5      (75) PVHGEE-NEDVDADDVSDYNYQASGNQ------DQKQKIAERMLTWRTNS
ZmCesA4      (76) AIRGEE-GDDTDAD--SDFNYLASGNE------DQKQKIADRMRSWRMNV
ZmCesA3      (1)  ----------------------------------------------------
ZmCesA2      (98) RVHGDD-EEDVDDLDNEFNYKQGNGK------GPSWQLQGDDADLSSSA
SeqIdNo.30   (94) RVAGDD-DEEDIDDLEHEFNIDDENQQRQLEGNMQNSQITEAMLHGRMSY
ZmCesA12     (1)  ----------------------------------MQNSQITEAMLHGRMSY
ZmCesA11     (59) ASEGTEAKEEVVENHHTAGGLRERVTMGSHLNDRQDEVSHARTMSSLSGI
ZmCesA10     (98) RVEGDEEGPEMDDFEDEFPAKS------------PKKPHEPVAFDVYSE
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ZmCesA1     (98)  RVHGDE-DEEDVDDLDNEFNYKQGSGK------GPEWQLQGDDADLSSSA
Consensus   (101) RV GDE EED VDD E EFNY                I E ML    MS

                                                                   200
                  151
ZmCesA9     (119) GGSGDVGRPKYDSGEIGLTKYDSGEIPRGYIPSVTNSQISGEIPGASPDH
ZmCesA8     (142) CRG---GDAHPGFSPVPNVPLLTNGQMVDDIPPEQHALVPSYMSGGGCG
ZmCesA7     (135) GRGGDPNGAPQAFQLNPNVPLLTNGQMVDDIPPDQHALVPSFVGGGG---
ZmCesA6     (106) CRGADLDGVPQPFHPIPNVPLLTNGQMVDDIPPEQHALVPSFVGGGG---
ZmCesA5     (118) RGS-DIGLAKYDSGEIGHGKYDSGEIPRGYIPSLTHSQISGEIPGASPDH
ZmCesA4     (117) GGSCDVGRPKYDSGEIGLTKYDSGEIPRGYIPSVTNSQISGEIPGASPDH
ZmCesA3     (1)   --------------------------------------------------
ZmCesA2     (141) RHDPHHRIPRLTSGQQ----------------IS-----GEIPDASPDR
SeqIdNo.30  (143) GRG---PDDGDGNNTPQIPPIITGSRSVPVSGEFPITNGYCHGEVSSSLH
ZmCesA12    (18)  GRG---PDDGDGNNTPQIPPIITGSRSVPVSGEFPITNGYGHGEVSSSLH
ZmCesA11    (109) GSELN--------------------------------------------
ZmCesA10    (136) NGE----------------------------------------------
ZmCesA1     (141) RHEPHHRIPRLTSGQQ----------------IS-----GEIPDASPDR
Consensus   (151) G                     T                G I  AS
                  201                                              250
ZmCesA9     (169) HMMSPTGNIGRRAPFPYMNHSSNPSRE-FSGSVGNVAWKERVDGWKMKQD
ZmCesA8     (189) KRIHPLPFA--DPNLPVQPRSMDPSKDLAAYGYGSVAWKERMEGWKQKQE
ZmCesA7     (182) KRIHPLPYA--DPSLPVQPRSMDPSKDLAAYGYGSVAWKERMENWKQRQE
ZmCesA6     (153) KRIHPLPYA--DPNLPVQPRSMDPSKDLAAYGYGSVAWKERMESWKQKQE
ZmCesA5     (167) MMSPVGNIGRRGHQFPYVNHSPNPSRE-FSGSLGNVAWKERVDGWKMK-D
ZmCesA4     (167) HMMSPTGNIGKRAPFPYVNHSPNPSRE-PSGSIGNVAWKERVDGWKMKQD
ZmCesA3     (1)   -------------------------------------------------
ZmCesA2     (169) HSIRSPTSSYVDPSVPVPVRIVDPSKDLNSYGLNSVDWKERVESWRVKQD
SeqIdNo.30  (190) KRIHPYPVS--EPGSAKWDE-----------KKEVSWKERMDDWKSKQG
ZmCesA12    (65)  KRIHPYPVS--EPGSAKWDE-----------KKEVSWKERMDDWKSKQG
ZmCesA11    (114) ------------DE--SGK-------------PIWKNRVESWKEKKN
ZmCesA10    (139) -HPAQKWRTGGQTLSSFTCSVAGKDLEAEREMEGSMEWKDRIDKWKTKQE
ZmCesA1     (169) HSIRSPTSSYVDPSVPVPVRIVDPSKDLNSYGLNSVDWKERVESWRVKQD
Consensus   (201)  I P   S  DP P       PSKD  S   G VAWKERVD WK KQD
                  251                                              300
ZmCesA9     (218) KGTIPMTNGTSIAPSEGRGVGDIDASTDYNMEDALLNDETRQPLSRKVPL
ZmCesA8     (237) RLQHVRS-----------EGGG--DWDGDDADLPLMDEARQQLSRKIPL
ZmCesA7     (230) RMHQTGN-----------DGG---GDDGDDADLPLMDEARQPLSRKIPL
ZmCesA6     (201) RMHQTRN-----------DGG---GDDGDDADLPLMDEARQPLSRKIPL
ZmCesA5     (215) KGAIPMTNGTSIAPSEGRGVADIDASTDYNMEDALLNDETRQPLSRKVPT
ZmCesA4     (216) KGTIPMTNGTSIAPSEGRGVGDIDASTDYNMEDALLNDETRQPLSRKVPL
ZmCesA3     (1)   ---------------------------------------PLSRIVPI
ZmCesA2     (219) KNMLQVTNKYPEARG----DMEGTGSNGE---DMQMVDDARLPLSKIVPI
SeqIdNo.30  (226) --ILG---------------GGA--DPEDMDADVALNDEARQPLSRKVSI
ZmCesA12    (101) --ILG---------------GGA--DPEDMDADVALNDEARQPLSRKVSI
ZmCesA11    (134) EKKASAKKTAAKAQP----P--P---VEEQIMDEKDETDAYEPLSRVIPI
ZmCesA10    (188) K-RGKLN-----------HDDSDDDDKNEDEYMLLAEARQPLWRKVPI
ZmCesA1     (219) KNMMQVTNKYPEARGG---DMEGTGSNGE---XMQMVDDARLPLSRIVPI
Consensus   (251) K  I               G     D    DL LMDEARQPLSRKVPI
                  301                                              350
ZmCesA9     (268) PSSRINPYRMVIVLRLIVLSIFLHYRITNPVRNAYPLWLLSVICEIWFAL
ZmCesA8     (273) SSSRINPYRMIIVIRLVVLGFFHYRVMHPAKDAFALWLISVICEIWFAM
ZmCesA7     (265) PSSQINPYRMIIIIRLVVIGFFHYRVMHPVNDAFALWLISVICEIWFAM
ZmCesA6     (236) PSSQINPYRMIIIIRLVVICFFHYRVMHPVPDAFALWLISVICEIWFAM
ZmCesA5     (265) PSSRINPYRMVIVLRLAVICIFLRYRITHPVNNAYPLWLLSVICEIWFAL
ZmCesA4     (266) PSSRINPYRMVIVLRLIVLSIFLHYRITNPVRNAYPLWLLSVICEIWFAL
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ZmCesA3      (9)  SPNELNLYRIVIVLRLIILCFFFQYFITHPVEDAYGLWLVSVICEVWFAL
ZmCesA2    (262)  SSNQLNLYRIVIILRLIILCFFFQYRISHPVRNAYGLWLVSVICEVWFAL
SeqIdNo.30 (257)  ASSKVNPYRMVIVVRLVVLAFFLRYRILHPVPDAIGLWLVSIICEIWFAI
ZmCesA12   (132)  ASSKVNPYRMVIVVRLVVIAFFLRYRILHPVPDAIGLWLVSIICEIWFAY
ZmCesA11   (175)  SKNKLTPYRAVIIMRLIVLGLFFHYRITNPVNSAFGLWMTSVICEIWFQF
ZmCesA10   (225)  PSSMINPYRIVIVLRLVVVCFFLKFRITTPATUAVPLWLASVICELWFAF
ZmCesA1    (263)  SSNQLNLYRVVIILRLIILCFFFQYRVSHPVRDAYGLWLVSVICEVWFAL
Consensus  (301)  SSSRINPYRMVIVLRLIVL FFF YRITHPV DAYGLWLVSVICEIWFAL
                  351                                              400
ZmCesA9    (318)  SWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAAVDIFVSTVDPMKE
ZmCesA8    (323)  SWILDQFPKWLFIERETYLDRLSLRFDKEGQPSQLAPIDFFVSTVDPTKE
ZmCesA7    (315)  SWILDQFPKWFPIERETYLDRLSLRFDKEGQPSQLAPIDFFVSTVDPLKE
ZmCesA6    (286)  SWILDQFPKWFPIERETYLDRLSLRFDKFGHPSQLAPVDFFVSTVDPMKE
ZmCesA5    (315)  SWILDQFPKWSPINRETYLDRLALRYDREGEPSQLAAVDIFVSTVDPMKE
ZmCesA4    (316)  SWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAPIDVFVSTVDPLKE
ZmCesA3     (59)  SWLLDQFPKWYPINRETYLDRLALRYDREGEPSQLAPIDVFVSTVDPLKE
ZmCesA2    (312)  SWILDQFPKWYPINRETYLDRLSLRYEREGEPSLLSAVDLFVSTVDPLKE
SeqIdNo.30 (307)  SWILDQFPKWFPIDRETYLDRLSLRYEREGEPSLLSAVDLFVSTVDPLKE
ZmCesA12   (182)  SWILDQFPKWFPIDRETYLDRLSLRYEREGEPSLLSAVDLFVSTVDPLKE
ZmCesA11   (225)  SWILDQFPKWYPINRETYVDRLIARYG-DGEESGLAPVDFFVSTVDPLKE
ZmCesA10   (275)  SWILOOLPKWAPVTRETYLDRLALRYDREGEACRLSPIDFFVSTVDPLKE
ZmCesA1    (313)  SWLLDQFPKWYPINRETYLDRLALRYDREGEPSQLAPIDVFVSTVDPLKE
Consensus  (351)  SWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAPVDIFVSTVDPLKE
                  401                       *                    450
ZmCesA9    (368)  PPLVTANFVLSILAVDYPVDKVSCYVSDDGAAMLTFDALAETSEFARKWV
ZmCesA8    (373)  PPLVTANTVLSILSVDYPVEKVSCYVSDDGAAMLTFEALSETSEFAKKWV
ZmCesA7    (365)  PPLVTTVTVLSILSVDYPVDKVSCYVSDDGAAMLTFEALSETSEFAKKWV
ZmCesA6    (336)  PPLVTANTVLSILSVDYPVDKVSCYVSDDGAAMLTFEALSETSEFARKWV
ZmCesA5    (365)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGAAMLTFDALSETSEFARKWV
ZmCesA4    (366)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGAAMLTFDALAETSEFARKWV
ZmCesA3    (109)  PPLITGNTVLSILAVDYPVDKVSCYVSDDCSAMETFEALSETAEFARKWV
ZmCesA2    (362)  PPLITANTVLSILAVDYPVDKVSCYVSDDCSAMLTFESLSETAEFARKWV
SeqIdNo.30 (357)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFESLSETAEFARKWV
ZmCesA12   (232)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFESLAETAEYARKWV
ZmCesA11   (274)  PPLITANTVLSILAVDYPVEKISCYVSDDGASMLLFDALSETAEFARKWV
ZmCesA10   (325)  PPLITANTVLSILAVDYPVDRVSCYVSDDGASMLTFESLSETAEFARKWV
ZmCesA1    (363)  PPLITANTVLSILSVDYPVDKVSCYVSDDGSAMLTFESLSETAEFARKWV
Consensus  (401)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGAAMLTFEALSETAEFARKWV
                  451                                            500
ZmCesA9    (418)  PFVKKYNIEPRAPEWYFSQKIDYLKDKVHPSFVKDRRAMKREYEEFKIRV
ZmCesA8    (423)  PFSKKENIEPRAPEWYFQQKIDYLKDKVAASFVRERRAMKREYEEFKVRI
ZmCesA7    (415)  PFCKRYNIEPRAPEWYFQQKIDYLKDKVAANFVRERRAMKREYEEFKVRI
ZmCesA6    (386)  PFCKRYSIEPRAPEWYFQQKIDYLKDKVAPNEVRERRAMKREYEEFKVRI
ZmCesA5    (415)  PFVKKYNIEPXAPEWYFAQKIDYLKDKVHPSFVKDRRAMKREYEEFKVRV
ZmCesA4    (416)  PFVKKYNIEPRAPEWYFSQKIDYLKDKVHPSFVKDRRAMKRECEEFKVRI
ZmCesA3    (159)  PFCKKHNIEPRAPEFYFAQKIDYLKDKIQPSFVKERRAMKREYEEFKIRI
ZmCesA2    (412)  PFCKKHNIEPRAPEFYFAQKIDYLKDKIQPSFVKERRAMKREYEEFKVRI
SeqIdNo.30 (407)  PFCKKFGIEPRAPEFYFSLKVDYLKDKVQPTFVQERRAMKREYEEFKVRI
ZmCesA12   (282)  PFCKKFGIEPRAPEFYFSLKVDYLKDKVQPTFVQERRAMKREYEEFKVRI
ZmCesA11   (324)  PFCKKYAIEPRAPEFYFSQKIDYLKDKIHPSFVKERRAMKRDYEEYKVRI
ZmCesA10   (375)  PFCKKFAVEPRAPEFYFSQKIDYLKDKVQPTFVKERRAMKREYEEFKVRI
ZmCesA1    (413)  PFCKKHNIEPRAPEFYFAQKIDYLKDKIQPSFVKERRAMKREYEEFKVRI
Consensus  (451)  PFCKKYNIEPRAPEFYFSQKIDYLKDKVQPSFVKERRAMKREYEEFKVRI
                  501                                            550
ZmCesA9    (468)  NGLVAKAQKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGN
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ZmCesA8    (473) NALVAKAQKVPEEGWTMQDGSPWPGNNVRDHPGMIQVFEGQSGGRLVEGN
ZmCesA7    (465) NALVAKAQKVPEEGWTMQDGTPWPGNNVRDHPGMIQVFLGQSGGLDCEGN
ZmCesA6    (436) NALVAKAQKVPEEGWTMQDGTPWPGNNVRDHPGMIQVFLGQSGGCLDVEGN
ZmCesA5    (465) NGLVAKAQKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSCGLDTEGN
ZmCesA4    (466) NGLVAKAQKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSCGLDTDGN
ZmCesA3    (209) DALVAKAQKIPEEGWTMADGTPWPGNNPRDHPGMIQVFLGHSGGLDTDGN
ZmCesA2    (462) NALVAIGMKVPEEGWIMADGTAWPGNNPRDHPGMIQVFLGHSCCHDTEGN
SeqIdNo.30 (457) NALVAIGMKVPAEGWIMKDGTPWPGNNTRDHPGMIQVFLGHSGGHDTEGN
ZmCesA12   (332) NADVAKAMKVPAEGWIMKDGTPWPGNNTRDHPGMIQVFLGETGARDFDGN
ZmCesA11   (374) NALVAKAQKTPDEGWIMQDGTPWPGNNPRDHPGMIQVFLGETGARDFDGN
ZmCesA10   (425) NALVAKAQKKPEEGWVMQDGTPWPGNNTRDHPGMIQVYLGNQGALDVEGH
ZmCesA1    (463) NALVAKAQKVPEEGWTMADGTAWPGNNPRDHPGMIQVFLGHSGGLDTDGN
Consensus  (501) NALVAKAQKVPEEGWIMQDGTPWPGNN RDHPGMIQVFLGHSGGLDTEGN
                                                                *600
                 551
ZmCesA9    (518) ELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYI
ZmCesA8    (523) ELPRLVYVSREKRPCYNHHKKAGAMNALVRVSAVLSNAAYLLNLDCDHYI
ZmCesA7    (515) ELPRLVYVSREKRPGYNHHKKAGAMNALVRVSAVLTNAPYLLNLDCDHYI
ZmCesA6    (486) ELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYI
ZmCesA5    (515) ELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYI
ZmCesA4    (516) ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNGAYLLNVDCDHYF
ZmCesA3    (259) ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNGAYLLNVDCDHYF
ZmCesA2    (512) ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNAPFMLNLDCDHYI
SeqIdNo.30 (507) ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNAPFMLNLDCDHYI
ZmCesA12   (382) ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNAPYILNLDCDHYV
ZmCesA11   (424) ELPRLVYVSREKRPGYQHHKKAGAMNALVRVSAVLTNAPFILNLDCDHYV
ZmCesA10   (475) ELPRLVYVSREKRPGYNHHKKAGAMNALIRVSAVLTNGAYLLNVDCDHYF
ZmCesA1    (513) ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNA YLLNLDCDHYI
Consensus  (551) ELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNA YLLNLDCDHYI
                                                                650
                 601
ZmCesA9    (568) NNSKALREAMCFLMDPNLGRSVCYVQFPQRFDGIDRNDRYANPNTVFFDI
ZmCesA8    (573) NNSKALKEAMCFMMDPLVGKKVCYVQFPQRFDGIDKNDRYANRNVVFFDI
ZmCesA7    (565) NNSKALKEAMCFMMDPLLGKKVCYVQFPQRFDGIDRHDRYANRNVVFFDI
ZmCesA6    (536) NNSKALKEAMCFMMDPLLGKKVCYVQFPQRFDGIDRHDRYANRNVVFFDI
ZmCesA5    (565) NNSKALREAMCFLMDPNLGRNVCYVQFPQRFDGIDRNDRYANRNTVFFDI
ZmCesA4    (566) NNSKALREAMCFLMDPNLGRSVCYVQFPQRFDGIDLHDRYANRNIVFFDI
ZmCesA3    (309) NSSKALREAMCFMMDPALGRKTCYVQFPQRFDGIDLHDRYANRNIVFFDI
ZmCesA2    (562) NNSKALREAMCFLMDPQVGRKVCYVQFPQRFDGIDVHDRYANRNTVFFDI
SeqIdNo.30 (557) NNSKALREAMCFLMDPQVGRKVCYVQFPQRFDGIDVHDRYANRNTVFFDI
ZmCesA12   (432) NNSKAVREAMCFMMDPTVGRDVCYVQFPQRFDGIDRSDRYANRNVVFFDV
ZmCesA11   (474) NNSKAVREAMCFMMDPTVGRDVCYVQFPQRFDGIDRSDRYANRNVVFFDV
ZmCesA10   (525) NNSKAVREAMCFLMDPQLGKKLCYVQFPQRFDGIDRHDRYANRNVVFFDI
ZmCesA1    (563) NSSKALREAMCFMMDPALGRKTCYVQFPQRFDGIDLHDRYANRNIVFFDI
Consensus  (601) NNSKALREAMCFMMDP LGRKVCYVQFPQRFDGIDRHDRYANRNVVFFDI
                                                                700
                 651
ZmCesA9    (618) NLRGLDGIQGPVYVGTGCVFNRTALYGYEPPIKQKKGG--------FLS
ZmCesA8    (623) NMKGLDGIQGPIYVGTGCVFRRQALYGYDAPKTKKPPSRTCNCWPKWCLS
ZmCesA7    (615) NMKGLDGIQGPIYVGTGCVFRRQALYGYDAPKTKKPPSRTCNCWPKWCIC
ZmCesA6    (586) NMKGLDGIQGPIYVGTGCVFRRQALYGYDAPKTKKPPSRTCNCWPKWCIC
ZmCesA5    (615) NLRGLDGIQGPVYVGTGCVFNRTALYGYEPPVKKKKPG---------PFS
ZmCesA4    (616) NLRGLDGIQGPVYVGTGCVFNRTALYGYEPPIKQKKGG--------FLS
ZmCesA3    (359) NMKGLDGIQGPVYVGTGCCFNRQALYGYDPVLTEADLEP------NIILK
ZmCesA2    (612) NMKGLDGIQGPVYVGTGCCFNRQALYGYDPVLTEADLEP------NIVVK
SeqIdNo.30 (607) NMKGLDGIQGPVYVGTGCVFRRQALYGYNPPKGPKRPK------MVTCDC
ZmCesA12   (482) NMKGLDGIQGPVYVGTGCVFRRQALYGYNPPKGPKRPK------MVTCDC
ZmCesA11   (524) NMKGLDGLQGPVYVGTGCCFNRQALYGYGPPSLPALPKS------SICSW
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ZmCesA10    (575)  NMKGLDGIQGPVYVGTGCVFNRQALYGYDPPRPEKRPKMTCDCWPSWCCC
ZmCesA1     (613)  NMKGLDGIQGPVYVGTGCCFNRQALYGYDPVLTEADLEP------NIVIK
Consensus   (651)  NMKGLDGIQGPVYVGTGCVFNRQALYGYDPP      K P          CI
                   701                                                   750

ZmCesA9     (659)  SLCGGRK----------------------------KGSKSKKGSDKKKSQK
ZmCesA8     (673)  CCCSRNK----------------------------NKKKTTKPKTEKKKRLFFK
ZmCesA7     (665)  CCCFGNR----------------------------KQKKTTKPKTEKKKLLPFK
ZmCesA6     (636)  CCCFGNRKTK-------------------------KKTKTSKPKFEKIKKLFKK
ZmCesA5     (656)  SLCGGRK----------------------------KTSKSKKSSEKKKSHR
ZmCesA4     (657)  SLCGGRK----------------------------KASKSKKGSDKKKSQK
ZmCesA3     (403)  SCCGGRK----------------------------KKDKSYIDS-KNRDMK
ZmCesA2     (656)  SCCGRRK----------------------------RKNKSYMDS-QSRIMK
SeqIdNo.30  (651)  CPCFCRK----------------------------KRKHAKDGLPEG------
ZmCesA12    (526)  CPCFGRK----------------------------KRKHAKDGLPEG------
ZmCesA11    (568)  CCCCCPK----------------------------KK-VERSEREINRDSR
ZmCesA10    (625)  CCCFGGGKRGKARKDKKGDGGEEPRRGLLGFYRKRSKKDKLGGGSVAGSK
ZmCesA1     (657)  SCCGRRK----------------------------KKNKSYMDS-QSRIMK
Consensus   (701)  CCC GRK                                  K KKE  KR  K
                   751                                                   800

ZmCesA9     (682)  HV----DSSVPVFNLEDIEEGVECAGFDDEKSLLMSQMSLEKRFGQSAAF
ZmCesA8     (699)  KA----ENPSPAYALGEIDEGAPG--ADIEKAGIVNQQKLEKKFGQSSVF
ZmCesA7     (691)  KE----ENQSPAYALGEIDEAAPG--AENEKAGIVNQQKLEKKFGQSSVF
ZmCesA6     (665)  KE-----NQAPAYALGEIDEAAPG--AENEKASIVNQQKLEKKFGQSSVF
ZmCesA5     (679)  HA----DSSVPVFNLEDIEEGIEGSQFDDEKSLLMSQMSLEKRFGQSAAF
ZmCesA4     (680)  HV----DSSVPVFNLEDIEEGVEGAGFDDEKSLLMSQMSLEKRFGQSAAF
ZmCesA3     (425)  RT----ESSAPIFNMEDIEEGFEG--YEDERSLLMSQKSLEKRFGQSPIF
ZmCesA2     (678)  RT----ESSAPIFNMEDIEEGIEG--YEDERSVLMSORKLEKRFGQSPIF
SeqIdNo.30  (670)  -------------------TADMG--VDSDKEMLMSHMNFEKRFGQSAAF
ZmCesA12    (545)  -------------------TADMG--VDSDKEMLMSHMNFEKRFGQSAAF
ZmCesA11    (590)  RE----DLESAIFNLREIDNYDEY----ERSMLISQMSFEKSFGLSSVF
ZmCesA10    (675)  KGGGLYKKHQRAFELEEIEEGLEG-YDELERSSLMSQKSPEKRFGQSPVF
ZmCesA1     (679)  RT----ESSAPIFNMEDIEEGIEG--YEDERSVLMSORKLEKRFGQSPIF
Consensus   (751)  K        E  APIFNLEDIEEG EG    D EKSLLMSQ  LEKRFCQSSVF
                   801                                                   850

ZmCesA9     (728)  VASTLMEYGGVPQ--SATRESLLKEAIHVISCGYEDKIEWGTEIGWIYGS
ZmCesA8     (743)  VASTLDENGGTLK--SASPASLLKEAIHVISCGYEDKTDWGKEIGWIYGS
ZmCesA7     (735)  VTSTLLENGGTLK--SASPASLLKEAIHVISCGYEDKTDWGKEIGWIYGS
ZmCesA6     (708)  VASTLLENGGTLK--SASPASLLKEAIHVISCGYEDKTGWGKDIGWIYGS
ZmCesA5     (725)  VASTLMEYGGVPQ--SATRESLLKEAIHVISCGYEDKTDWGTEIGWIYGS
ZmCesA4     (726)  VASTLMEYGGVPQ--SATRESLLKEAIHVISCGYEDKTEWGTEIGWIYGS
ZmCesA3     (469)  IASTFMTQGGIPP--STNPGSLLKEAIHVISCGYEDKTEWGKEIGWIYGS
ZmCesA2     (722)  IASTFMTQGGIPP--STNPASLLKEAIHVISCGYEDKTEWGKEIGWIYGS
SeqIdNo.30  (699)  VTSTLMEEGGVPP--SSSPAALLKEAIHVISCGYEDKTDWGLELGWIYGS
ZmCesA12    (574)  VTSTLMEEGGVPP--SSSPAALLKEAIHVISCGYEDKTDWGLELGWIYGS
ZmCesA11    (631)  IESTLMENGGVPES--ANPSTLIKEAIHVISCGYEEKTEWGKEIGWIYGS
ZmCesA10    (724)  IASTLVEDGGEPQGAAADPAALLKEAIHVISCGYEEKTEWGKEIGWIYGS
ZmCesA1     (723)  IASTFMTQGGIPP--STNPASLLKEAIHVISCGYEDKTEWGKEIGWIYGS
Consensus   (801)  VASTLMENGGVP   SASPASLLKEAIHVISCGYEDKTEWGKEIGWIYGS
                   851                                            *  +  900

ZmCesA9     (776)  VTEDILTGFKMHARGWRSIYCMPKRPAFKGSAPINLSDRLNQVLRWALGS
ZmCesA8     (791)  ITEDILTGFKMHCHGWRSIYCIPKRPAFKGSAPLNLSDRLHQVLRWALGS
ZmCesA7     (783)  VTEDILTGFKMHCHGWRSIYCIPKRVAFKGSAPLNLSDRLHQVLRWALGS
ZmCesA6     (756)  VTEDILTGFKMHCHGWRSIYCIPKRAAFKGSAPLNLSDRFHQVLRWALGS
ZmCesA5     (773)  VTEDILTGFKMHARGWRSIYCMPKRPAFKGSAPINLSDRLNQVLRWALGS
ZmCesA4     (774)  VTEDILTGFKMHARGWRSIYCMPKRPAFKGSAPINLSDRLNQVLRWALGS
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    ZmCesA3      (517)  VTEDILTGFKMHARGWISIYCMPLRPCFKGSAPINLSDRLNQVLRWALGS
    ZmCesA2      (770)  VTEDILTGFKMHARGWQSIYCMPPRPCFKGSAPINLSDRLNQVLRWALGS
  SeqIdNo.30     (747)  ITEDILTGFKMHCRGWRSVYCMPKRAAFKGSAPINLSDRLNQVLRWALGS
    ZmCesA12     (622)  ITEDILTGFKMHCRGWRSVYCMPKRAAFKGSAPINLSDRLNQVLRWALGS
    ZmCesA11     (679)  VTEDILTGFKMHCRGWRSIYCMPVRPAFKGSAPINLSDRLHQVLRWALVS
    ZmCesA10     (774)  VTEDILTGFKMHCRGWKSVYCTPTRPAFKGSAPINLSDRLHQVLRWALGS
    ZmCesA1      (771)  VTEDILTGFKMHARGWQSIYCMPPRPCFKGSAPINLSDRLNQVLRWALGS
    Consensus    (851)  VTEDILTGFKMHCRGWRSIYCMPKRPAFKGSAPINLSDRLNQVLRWALGS
                        901                                            950
    ZmCesA9      (826)  VEILFSRHCPLWYGYGGR-LKFLERFAYINTTIYPLTSLPLLIYCILPAI
    ZmCesA8      (841)  VEIFFSXHCPLWYGYGGG-LKFLERFSYINSIVYPWTSIPLLAYCTLPAI
    ZmCesA7      (833)  IEIFFSNHCPLWYGYGCG-LKFLERFSYINSIVYPWTSIPLLAYCTLPAI
    ZmCesA6      (806)  IEILFSNHCPLWYGYGGG-LKFLERFSYINSIVYPWTSIPLLAYCTLPAI
    ZmCesA5      (823)  IEILFSRHCPIWYGYGGR-LKFLERFAYINTTIYPLTSIPLLIYCILPAI
    ZmCesA4      (824)  VEILFSRHCPLWYGYGGR-LKFLERFAYINTTIYPLTSIPLLIYCILPAI
    ZmCesA3      (567)  VEILLSRHCPIWYGYNGR-LKLLERLAYINTIVYPITSIPLIAYCVLPAI
    ZmCesA2      (820)  VEILLSRHCPIWYGYNGR-LKLLERLAYINTIVYPITSVPLIAYCVLPAI
  SeqIdNo.30     (797)  VEIFFSRHSPLLYGYKNGNLKWLERFAYINTTIYPFTSLPLLAYCTLPAV
    ZmCesA12     (672)  VEIFFSRHSPLLYGYKNGNLKWLERFAYINTTIYPFTSLPLLAYCTLPAV
    ZmCesA11     (729)  VEIFFSRHCPLWYGYGGGRLKWLQRLSYINTIVYPFTSLPLVAYCCLPAI
    ZmCesA10     (824)  VEIFMSRHCPLRYAYGGR-LKWLERFAYTNTIVYPFTSIPLLAYCTIPAV
    ZmCesA1      (821)  VEILLSRHCPIWYGYNGR-LKLLERLAYINTIVYPITSIPLIAYCVLPAI
    Consensus    (901)  VEILFSRHCPLWYGYGGR LKFLERFAYINTIVYPFTSIPLLAYC LPAI
                        951                                            1000
    ZmCesA9      (875)  CLLTGKFIIPEISNFASIWFISLFISIFATGILEMRWSGVCIDEWWRNEQ
    ZmCesA8      (890)  CLLTGKFITPELTNVASIWFMALFICISVTGILEMRWSGVCIDDWWRNEQ
    ZmCesA7      (882)  CLLTGKFITPELNNVASLWFMSLFICIFAISILEMRWSGVCIDDWWRNEQ
    ZmCesA6      (855)  CLLTGKFITPELNNVASLWFMSLFICIFATSILEMRWSGVGIDDWWRNEQ
    ZmCesA5      (872)  CLLTGKFIIPKISNLESVWRISLFISIFATGILEMRWSGVGIDEWWRNEQ
    ZmCesA4      (873)  CLLTGKFIIPEISNFASIWFISLFISIFATGILEMRWSGVGIDEWWRNEQ
    ZmCesA3      (616)  CLLTNKFIIPAISNYAGAFPILLFASIFATGILELRWSGVGIEDWWRNEQ
    ZmCesA2      (869)  CLLTNKFIIPEISNYAGMFFILLFASIFATGILELRWSGVGIEDWWRNEQ
  SeqIdNo.30     (847)  CLLTGKFIMPSISTFASLFCIALFMSIFATGILEMRWSGVSIEEWWRNEQ
    ZmCesA12     (722)  CLLTGKFIMPSISTFASLFFIALFMSIFATGILEMRWSGIGIEDWWRNEQ
    ZmCesA11     (779)  CLLTCKFIIPTLSNAATIWFLGLFMSIIVTSVLELRWSGVSIEDWWRNEQ
    ZmCesA10     (873)  CLLTGKFIIPTLNNLASIWPTALFLGEIAISVLELRWSGVSIEDWWRNEQ
    ZmCesA1      (870)  CLLTNKFIIPEISNYAGMFFILLFASIFAKGILELRWSGVGIEDWWRNEQ
    Consensus    (951)  CLLTGKFIIPEISNFASIWFISLFISIFATGILEMRWSGVGIEDWWRNEQ
                        1001                                           1050
    ZmCesA9      (925)  FWVIGGTSAHLFAVFQGLLKVLAGIDTNFTVTSKAS-DEDGDFARLYMFK
    ZmCesA8      (940)  FWVIGGVSAHLFAVFQGLLKVFAGIDTSFIVTSKAG--DDEEFSELYTFK
    ZmCesA7      (932)  FWVIGGVSSHLFAVFQGLLRVIAGVDTSFIVTSKGG--DDEEFSELYTFK
    ZmCesA6      (905)  FWVIGGVSSHLFAVFQGLLKVIAGVDTSFIVTSKGG--DDEEFAELYMFK
    ZmCesA5      (922)  FWVIGGISAHLFAVFQGLLKVLAGIDTSFIVTSKAT-DEDGDFAELYMFK
    ZmCesA4      (923)  FWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKAT-DDDGDFAELYVFK
    ZmCesA3      (666)  FWVIGGTSAHLFAVFQGLLKVLAGIDTNFTVTSKAS-DEDGDFAELYVFK
    ZmCesA2      (919)  FWVIGGTSAHLFAVFQGLLKVLAGIDTNFIVTSKATGDEDDEFAELYAFK
  SeqIdNo.30     (897)  FWVIGGVSAHLFAVVQGLLKVLAGIDTNFIVTSKATGDEDDEFAELYAFK
    ZmCesA12     (772)  FWVIGGVSAHLFAVVQGLLKVLAGIDTNFIVTSKATGDEDDEFAELYAFK
    ZmCesA11     (829)  FWVIGGVSAHLFAVFQGILKMIAGIDTNFIVTAKAT--DDTEFGELYLFK
    ZmCesA10     (923)  FWVIGGVSAHLFAVFQGFLKVLGGVDTSFIVSKAAGDEADAFGDLVLFK
    ZmCesA1      (920)  FWVIGGTSAHLFAVFQGLLKVLAGIDTNFTVTSKAS-DEDGDFAELYVFK
    Consensus    (1001) FWVIGGVSAHLFAVFQGLLKVLAGIDTNFTVTSKAT DED DFAELYMFK
                        1051                                           1100
    ZmCesA9      (974)  WTTLLIPPTTILIINLVGVVAGISYAINSGYQSWGPLFGKLFFAFWVIVH
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PAGE 26/27 * RCVD AT 6/10/2005 9:31:42 AM [Eastern Daylight Time] * SVR:USPTO-EFXRF-1/1 * DNIS:8729306 * CSID:515 334 6883 * DURATION (mm-ss):11-54

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ZmCesA8     (988)  WTTLLIPPTTLLLLNFIGVVAGISNAINNGYESWGPLFGKLFFAFWVIVH
ZmCesA7     (980)  WTTLLIPPTTLLLLNFIGVVAGVSNAINNGYESWGPLFGKLFFAFWVIVH
ZmCesA6     (953)  WTTLLIPPTTELLLNFIGVVAGISNAINNGYESWGPLFGKLFFAFWVIVH
ZmCesA5     (971)  WTTLLIPPTTILIINLVGVVAGISYAINSGYQSWGPLFGKLFFAFWVIVH
ZmCesA4     (972)  WFTLLIPPTTILIINLVGVVAGISYAINSGYQSWGPLFGKLFFAIWVILH
ZmCesA3     (715)  WTTLLTPPTTVLVINLVGIVAGVSYAINSGYQSWGPLFGKLFFSIWVILH
ZmCesA2     (968)  WTSLLIPPTTVLVINLVGMVAGISYAINSGYQSWGPLFGKLFFSIWVILH
SeqIdNo.30  (947)  WTTLLIPPTTLLIINVIGVVAGISDAINNGYQSWGPLFGKLFFAFWVIVH
ZmCesA12    (822)  WTTLLIPPTTLLIINVIGVVAGISDAINNGYQSWGPLFGKLFFAFWVIVH
ZmCesA11    (877)  WTTVLIPPTSILVINLVGVVAGFSAALNSGYESWGPLFGRVEFAMWVIMH
ZmCesA10    (973)  WTTLLVPPTTLIIINMVGIVAGVSDAVNNGYGSWGPLFGKLFFSFWVIVH
ZmCesA1     (969)  WTSLLIPPTTVLVINLVGMVAGISYAINSGYQSWGPLFGKLFFSIWVILH
Consensus   (1051) WTTLLIPPTTLLIINLVGVVAGIS AINSGYQSWGPLFGKLFFAFWVIVH
                   1101                                            1150
ZmCesA9     (1024) LYPFLKGLMGRQNRTPTIVVVWAILLASIFSLLWVRIDPFTNRVTCPD--
ZmCesA8     (1038) LYPFLKGLVGRQNRTPTIVIVWSILLASIFSLLWVRIDPFLAKSNGPL--
ZmCesA7     (1030) LYPFLKGLVGRQNRTPTIVIVWSILLASIFSLLWVRIDPFLAKDDGPL--
ZmCesA6     (1003) LYPFLKGLVGRQNRTPTIVIVWSILLASIFSLLWVRIDPFLAKDDCPL--
ZmCesA5     (1021) LYPFLKGLMGKQNRTPTIVVVWAILLASIFSLMWVRIDPFTTRVTGPD--
ZmCesA4     (1022) LYPFLKGLMGRQNRTPTIVVVWAILLASIFSLLWVRIDPFTTRVTGPD--
ZmCesA3     (765)  LYPFLKGLMGKQNRTPTIVIVWSVLLASIFSLLWVKIDPFISPTQKALS-
ZmCesA2     (1018) LYPFLKGLMGRQNRTPTIVIVWSILLASIFSLLWKIDPFISPTQKAAA-
SeqIdNo.30  (997)  LYPFLKGLMGRQNRTPTVVVWSILLASIFSLLWVRIDPFIVRTKGPD--
ZmCesA12    (872)  LYPFLKGLMGRQNRTPTVVVWSILLASVFSLLWVKIDPFVGGTETVNTN
ZmCesA11    (927)  LYPFLKGLMGRQNRTPTIVVLWSILLASIFSDVWVRIDPFIPKAKGPI--
ZmCesA10    (1023) LYPFLKGLMGRQNRTPTIVVLWSILLASIFSLLWVKIDPFISPTQKAAA-
ZmCesA1     (1019) LYPFLKGLMGRQNRTPTIVVVWSILLASIFSLLWVRIDPFI RT GP
Consensus   (1101) LYPFLKGLMGRQNRTPTIVVVWSILLASIFSLLWVRIDPFI RT GP
                   1151                            1181
ZmCesA9     (1072) -------------------TRTCGINC------
ZmCesA8     (1086) -------------------LEECGLDCN-----
ZmCesA7     (1078) -------------------LEECGLDCN-----
ZmCesA6     (1051) -------------------LEECGLDCN-----
ZmCesA5     (1069) -------------------IAKCGINC------
ZmCesA4     (1070) -------------------TQTCGINC------
ZmCesA3     (814)  -------------------RGQCGVNC------
ZmCesA2     (1067) -------------------LGQCGVNC------
SeqIdNo.30  (1045) -------------------VRQCGINC------
ZmCesA12    (920)  -------------------VRQCGINC------
ZmCesA11    (977)  NCNTHLLIHHRSAAVVPRRTCPWCCKRGLPA
ZmCesA10    (1071) -------------------EKPCGVEC------
ZmCesA1     (1068) -------------------LGQCGVNC------
Consensus   (1151)                    L  CGINC
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